

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(I) APPLICANT: DUAN, D. ROXANNE
SHILATIFARD, ALI
CONAWAY, JOAN W.
CONAWAY, RONALD C.

(ii) TITLE OF INVENTION: ELL2, A New Member of an ELL Family of
RNA Polymerase II Elongation Factors

(iii) NUMBER OF SEQUENCES: 34

(iv) CORRESPONDENCE ADDRESS:

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(E) COUNTRY: USA
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To be assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/038,447
(B) FILING DATE: 19-FEB-1997

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: 1488.0880001

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 94..2013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGTGGCGGC GGGTGCAGAA GCCCAAGCAG CGCGGCCGCA GTGGAGGCTA GAGCCGGAGC	60
GGCGGCGGCG GCGGCACCCC GGGGAGGTTT AAG ATG GCG GCG GGG GGG ACA GGG	114
Met Ala Ala Gly Gly Thr Gly	
1 5	
GGC CTG CGG GAG GAG CAG CGC TAT GGG CTG TCG TGC GGA CGG CTG GGG	162
Gly Leu Arg Glu Glu Gln Arg Tyr Gly Leu Ser Cys Gly Arg Leu Gly	
10 15 20	
CAG GAC AAC ATC ACC GTA CTG CAT GTG AAG CTC ACC GAG ACG GCG ATC	210
Gln Asp Asn Ile Thr Val Leu His Val Lys Leu Thr Glu Thr Ala Ile	
25 30 35	
CGG GCG CTC GAG ACT TAC CAG AGC CAC AAG AAT TTA ATT CCT TTT CGA	258
Arg Ala Leu Glu Thr Tyr Gln Ser His Lys Asn Leu Ile Pro Phe Arg	
40 45 50 55	
CCT TCA ATC CAG TTC CAA GGA CTC CAC GGG CTT GTC AAA ATT CCC AAA	306
Pro Ser Ile Gln Phe Gln Gly Leu His Gly Leu Val Lys Ile Pro Lys	
60 65 70	
AAT GAT CCC CTC AAT GAA GTT CAT AAC TTT AAC TTT TAT TTG TCA AAT	354
Asn Asp Pro Leu Asn Glu Val His Asn Phe Asn Phe Tyr Leu Ser Asn	
75 80 85	
GTG GGC AAA GAC AAC CCT CAG GGC AGC TTT GAC TGC ATC CAG CAA ACA	402
Val Gly Lys Asp Asn Pro Gln Gly Ser Phe Asp Cys Ile Gln Gln Thr	
90 95 100	
TTC TCC AGC TCT GGA GCC TCC CAG CTC AAT TGC CTG GGA TTT ATA CAA	450
Phe Ser Ser Ser Gly Ala Ser Gln Leu Asn Cys Leu Gly Phe Ile Gln	
105 110 115	
GAT AAA ATT ACA GTG TGT GCA ACA AAC GAC TCG TAT CAG ATG ACA CGA	498
Asp Lys Ile Thr Val Cys Ala Thr Asn Asp Ser Tyr Gln Met Thr Arg	
120 125 130 135	
GAA AGA ATG ACC CAG GCA GAG GAG GAA TCC CGC AAC CGA AGC ACA AAA	546
Glu Arg Met Thr Gln Ala Glu Glu Glu Ser Arg Asn Arg Ser Thr Lys	
140 145 150	
GTT ATC AAA CCC GGT GGA CCA TAT GTA GGG AAA AGA GTG CAA ATT CGG	594
Val Ile Lys Pro Gly Gly Pro Tyr Val Gly Lys Arg Val Gln Ile Arg	
155 160 165	
AAA GCA CCT CAA GCT GTT TCA GAT ACA GTT CCT GAG AGG AAA AGG TCA	642
Lys Ala Pro Gln Ala Val Ser Asp Thr Val Pro Glu Arg Lys Arg Ser	
170 175 180	
ACC CCC ATG AAC CCT GCA AAT ACA ATT CGA AAG ACA CAT AGC AGC AGC	690
Thr Pro Met Asn Pro Ala Asn Thr Ile Arg Lys Thr His Ser Ser Ser	
185 190 195	
ACC ATC TCT CAG AGG CCA TAC AGG GAC AGG GTG ATT CAC TTA CTG GCC	738
Thr Ile Ser Gln Arg Pro Tyr Arg Asp Arg Val Ile His Leu Leu Ala	
200 205 210 215	
CTG AAG GCC TAC AAG AAA CCG GAG CTA CTT GCT AGA CTC CAG AAA GAT	786

Leu	Lys	Ala	Tyr	Lys	Lys	Pro	Glu	Leu	Leu	Ala	Arg	Leu	Gln	Lys	Asp	
				220					225					230		
GGT	GTC	AAT	CAA	AAA	GAC	AAG	AAC	TCC	CTG	GGA	GCA	ATT	CTG	CAA	CAG	834
Gly	Val	Asn	Gln	Lys	Asp	Lys	Asn	Ser	Leu	Gly	Ala	Ile	Leu	Gln	Gln	
			235					240					245			
GTA	GCC	AAT	CTG	AAT	TCT	AAG	GAC	CTC	TCA	TAT	ACC	TTA	AAG	GAT	TAT	882
Val	Ala	Asn	Leu	Asn	Ser	Lys	Asp	Leu	Ser	Tyr	Thr		Leu	Lys	Asp	
			250				255					260				
GTT	TTT	AAA	GAG	CTT	CAA	AGA	GAC	TGG	CCT	GGA	TAC	AGT	GAA	ATA	GAC	930
Val	Phe	Lys	Glu	Leu	Gln	Arg	Asp	Trp	Pro	Gly	Tyr	Ser	Glu	Ile	Asp	
	265						270					275				
AGA	CGG	TCA	TTG	GAG	TCA	GTG	CTC	TCT	AGA	AAA	CTA	AAT	CCG	TCT	CAG	978
Arg	Arg	Ser	Leu	Glu	Ser	Val	Leu	Ser	Arg	Lys	Leu	Asn	Pro	Ser	Gln	
	280					285				290					295	
AAT	GCT	ACA	GGC	ACC	AGC	CGT	TCA	GAA	TCT	CCT	GTA	TGT	TCT	AGT	AGA	1026
Asn	Ala	Thr	Gly	Thr	Ser	Arg	Ser	Glu	Ser	Pro	Val	Cys	Ser	Ser	Arg	
				300					305					310		
GAT	GCT	GTA	TCT	TCT	CCT	CAG	AAA	CGG	CTT	TTG	GAT	TCA	GAG	TTT	ATT	1074
Asp	Ala	Val	Ser	Ser	Pro	Gln	Lys	Arg	Leu	Leu	Asp	Ser	Glu	Phe	Ile	
			315					320					325			
GAT	CCT	TTA	ATG	AAT	AAA	AAA	GCC	CGA	ATA	TCT	CAC	CTG	ACG	AAC	AGA	1122
Asp	Pro	Leu	Met	Asn	Lys	Lys	Ala	Arg	Ile	Ser	His	Leu	Thr	Asn	Arg	
			330				335					340				
GTA	CCA	CCA	ACA	CTA	AAT	GGT	CAT	TTG	AAT	CCC	ACC	AGT	GAA	AAA	TCG	1170
Val	Pro	Pro	Thr	Leu	Asn	Gly	His	Leu	Asn	Pro	Thr	Ser	Glu	Lys	Ser	
			345			350					355					
GCT	GCA	GGC	CTC	CCA	CTG	CCC	CCT	GCG	GCT	GCT	GCC	ATC	CCC	ACC	CCT	1218
Ala	Ala	Gly	Leu	Pro	Leu	Pro	Pro	Ala	Ala	Ala	Ala	Ile	Pro	Thr	Pro	
	360				365					370					375	
CCA	CCG	CTG	CCT	TCA	ACC	TAT	CTG	CCC	ATC	TCA	CAT	CCT	CCT	CAG	ATT	1266
Pro	Pro	Leu	Pro	Ser	Thr	Tyr	Leu	Pro	Ile	Ser	His	Pro	Pro	Gln	Ile	
				380				385						390		
GTA	AAT	TCT	AAC	TCC	AAC	TCC	CCT	AGC	ACT	CCA	GAA	GGC	CGG	GGG	ACT	1314
Val	Asn	Ser	Asn	Ser	Asn	Ser	Pro	Ser	Thr	Pro	Glu	Gly	Arg	Gly	Thr	
			395				400						405			
CAA	GAC	CTA	CCT	GTT	GAC	AGT	TTT	AGT	CAA	AAC	GAT	AGT	ATC	TAT	GAG	1362
Gln	Asp	Leu	Pro	Val	Asp	Ser	Phe	Ser	Gln	Asn	Asp	Ser	Ile	Tyr	Glu	
			410				415					420				
GAC	CAG	CAA	GAC	AAA	TAT	ACC	TCT	AGG	ACT	TCT	CTG	GAA	ACC	TTA	CCC	1410
Asp	Gln	Gln	Asp	Lys	Tyr	Thr	Ser	Arg	Thr	Ser	Leu	Glu	Thr	Leu	Pro	
			425			430					435					
CCT	GGT	TCC	GTT	CTA	CTA	AAG	TGT	CCA	AAG	CCT	ATG	GAA	GAA	AAC	CAT	1458
Pro	Gly	Ser	Val	Leu	Leu	Lys	Cys	Pro	Lys	Pro	Met	Glu	Glu	Asn	His	
					445					450				455		
TCA	ATG	TCT	CAC	AAA	AAG	TCC	AAA	AAG	AAG	TCT	AAA	AAA	CAT	AAG	GAA	1506
Ser	Met	Ser	His	Lys	Lys	Ser	Lys	Lys	Lys	Ser	Lys	Lys	His	Lys	Glu	
				460				465						470		

AAG GAC CAA ATA AAA AAG CAC GAC ATT GAG ACT ATT GAG GAA AAG GAG	1554
Lys Asp Gln Ile Lys Lys His Asp Ile Glu Thr Ile Glu Glu Lys Glu	
475 480 485	
GAA GAT CTT AAG AGA GAA GAG GAA ATT GCC AAG CTA AAT AAC TCC AGT	1602
Glu Asp Leu Lys Arg Glu Glu Glu Ile Ala Lys Leu Asn Asn Ser Ser	
490 495 500	
CCA AAT TCC AGT GGA GGA GTT AAA GAG GAT TGC ACT GCC TCC ATG GAA	1650
Pro Asn Ser Ser Gly Gly Val Lys Glu Asp Cys Thr Ala Ser Met Glu	
505 510 515	
CCT TCA GCA ATT GAA CTC CCA GAT TAT TTG ATA AAA TAT ATC GCT ATC	1698
Pro Ser Ala Ile Glu Leu Pro Asp Tyr Leu Ile Lys Tyr Ile Ala Ile	
520 525 530 535	
GTC TCC TAT GAG CAA CGC CAG AAT TAT AAG GAT GAC TTC AAT GCA GAG	1746
Val Ser Tyr Glu Gln Arg Gln Asn Tyr Lys Asp Asp Phe Asn Ala Glu	
540 545 550	
TAT GAT GAG TAC AGA GCT TTG CAT GCC AGG ATG GAG ACT GTA GCT AGA	1794
Tyr Asp Glu Tyr Arg Ala Leu His Ala Arg Met Glu Thr Val Ala Arg	
555 560 565	
AGA TTT ATC AAA CTA GAT GCA CAA AGA AAG CGC CTT TCT CCA GGC TCA	1842
Arg Phe Ile Lys Leu Asp Ala Gln Arg Lys Arg Leu Ser Pro Gly Ser	
570 575 580	
AAA GAG TAT CAG AAT GTT CAT GAA GAA GTC TTA CAA GAA TAT CAG AAG	1890
Lys Glu Tyr Gln Asn Val His Glu Glu Val Leu Gln Glu Tyr Gln Lys	
585 590 595	
ATA AAG CAG TCT AGT CCC AAT TAC CAT GAA GAA AAA TAC AGA TGT GAA	1938
Ile Lys Gln Ser Ser Pro Asn Tyr His Glu Glu Lys Tyr Arg Cys Glu	
600 605 610 615	
TAT CTT CAT AAC AAG CTG GCT CAC ATC AAA AGG CTA ATA GGT GAA TTT	1986
Tyr Leu His Asn Lys Leu Ala His Ile Lys Arg Leu Ile Gly Glu Phe	
620 625 630	
GAC CAA CAG CAA GCA GAG TCA TGG TCC TAGAACTCTG CTTGGACCAG	2033
Asp Gln Gln Gln Ala Glu Ser Trp Ser	
635 640	
AAGATGTGAA TAAACTTAAG CTTATTTATT TAAAATTCCA AATGAGTTGC TCTAGATTCT	2093
AAAAAGGTGA AACTTTGGCT GTTGAAAGTT TCAGTATTAG TAAACT	2139

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 640 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Ala	Gly	Gly	Thr	Gly	Gly	Leu	Arg	Glu	Glu	Gln	Arg	Tyr	Gly
1				5				10						15	

Leu	Ser	Cys	Gly 20	Arg	Leu	Gly	Gln	Asp 25	Asn	Ile	Thr	Val	Leu 30	His	Val
Lys	Leu	Thr 35	Glu	Thr	Ala	Ile	Arg 40	Ala	Leu	Glu	Thr	Tyr 45	Gln	Ser	His
Lys	Asn 50	Leu	Ile	Pro	Phe	Arg 55	Pro	Ser	Ile	Gln	Phe 60	Gln	Gly	Leu	His
Gly 65	Leu	Val	Lys	Ile	Pro 70	Lys	Asn	Asp	Pro	Leu 75	Asn	Glu	Val	His	Asn 80
Phe	Asn	Phe	Tyr	Leu 85	Ser	Asn	Val	Gly	Lys 90	Asp	Asn	Pro	Gln	Gly 95	Ser
Phe	Asp	Cys	Ile 100	Gln	Gln	Thr	Phe	Ser 105	Ser	Ser	Gly	Ala	Ser 110	Gln	Leu
Asn	Cys 115	Leu	Gly	Phe	Ile	Gln	Asp 120	Lys	Ile	Thr	Val	Cys 125	Ala	Thr	Asn
Asp	Ser 130	Tyr	Gln	Met	Thr	Arg 135	Glu	Arg	Met	Thr	Gln 140	Ala	Glu	Glu	Glu
Ser 145	Arg	Asn	Arg	Ser	Thr 150	Lys	Val	Ile	Lys	Pro 155	Gly	Gly	Pro	Tyr	Val 160
Gly	Lys	Arg	Val 165	Gln	Ile	Arg	Lys	Ala	Pro 170	Gln	Ala	Val	Ser	Asp 175	Thr
Val	Pro	Glu	Arg 180	Lys	Arg	Ser	Thr	Pro 185	Met	Asn	Pro	Ala	Asn 190	Thr	Ile
Arg	Lys	Thr 195	His	Ser	Ser	Ser	Thr 200	Ile	Ser	Gln	Arg	Pro 205	Tyr	Arg	Asp
Arg	Val 210	Ile	His	Leu	Leu	Ala 215	Leu	Lys	Ala	Tyr	Lys 220	Lys	Pro	Glu	Leu
Leu 225	Ala	Arg	Leu	Gln	Lys 230	Asp	Gly	Val	Asn	Gln 235	Lys	Asp	Lys	Asn	Ser 240
Leu	Gly	Ala	Ile 245	Leu	Gln	Gln	Val	Ala	Asn 250	Leu	Asn	Ser	Lys	Asp 255	Leu
Ser	Tyr	Thr 260	Leu	Lys	Asp	Tyr	Val	Phe 265	Lys	Glu	Leu	Gln	Arg 270	Asp	Trp
Pro	Gly	Tyr 275	Ser	Glu	Ile	Asp	Arg 280	Arg	Ser	Leu	Glu	Ser 285	Val	Leu	Ser
Arg	Lys 290	Leu	Asn	Pro	Ser	Gln 295	Asn	Ala	Thr	Gly	Thr 300	Ser	Arg	Ser	Glu
Ser 305	Pro	Val	Cys	Ser	Ser	Arg	Asp	Ala	Val	Ser 315	Ser	Pro	Gln	Lys	Arg 320
Leu	Leu	Asp	Ser 325	Glu	Phe	Ile	Asp	Pro	Leu 330	Met	Asn	Lys	Lys	Ala 335	Arg
Ile	Ser	His 340	Leu	Thr	Asn	Arg	Val	Pro 345	Pro	Thr	Leu	Asn	Gly 350	His	Leu

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Asn Pro Thr Ser Glu Lys Ser Ala Ala Gly Leu Pro Leu Pro Pro Ala
355                               360                               365

Ala Ala Ala Ile Pro Thr Pro Pro Pro Leu Pro Ser Thr Tyr Leu Pro
370                               375                               380

Ile Ser His Pro Pro Gln Ile Val Asn Ser Asn Ser Asn Ser Pro Ser
385                               390                               395                               400

Thr Pro Glu Gly Arg Gly Thr Gln Asp Leu Pro Val Asp Ser Phe Ser
405                               410                               415

Gln Asn Asp Ser Ile Tyr Glu Asp Gln Gln Asp Lys Tyr Thr Ser Arg
420                               425                               430

Thr Ser Leu Glu Thr Leu Pro Pro Gly Ser Val Leu Leu Lys Cys Pro
435                               440                               445

Lys Pro Met Glu Glu Asn His Ser Met Ser His Lys Lys Ser Lys Lys
450                               455                               460

Lys Ser Lys Lys His Lys Glu Lys Asp Gln Ile Lys Lys His Asp Ile
465                               470                               475                               480

Glu Thr Ile Glu Glu Lys Glu Glu Asp Leu Lys Arg Glu Glu Glu Ile
485                               490                               495

Ala Lys Leu Asn Asn Ser Ser Pro Asn Ser Ser Gly Gly Val Lys Glu
500                               505                               510

Asp Cys Thr Ala Ser Met Glu Pro Ser Ala Ile Glu Leu Pro Asp Tyr
515                               520                               525

Leu Ile Lys Tyr Ile Ala Ile Val Ser Tyr Glu Gln Arg Gln Asn Tyr
530                               535                               540

Lys Asp Asp Phe Asn Ala Glu Tyr Asp Glu Tyr Arg Ala Leu His Ala
545                               550                               555                               560

Arg Met Glu Thr Val Ala Arg Arg Phe Ile Lys Leu Asp Ala Gln Arg
565                               570                               575

Lys Arg Leu Ser Pro Gly Ser Lys Glu Tyr Gln Asn Val His Glu Glu
580                               585                               590

Val Leu Gln Glu Tyr Gln Lys Ile Lys Gln Ser Ser Pro Asn Tyr His
595                               600                               605

Glu Glu Lys Tyr Arg Cys Glu Tyr Leu His Asn Lys Leu Ala His Ile
610                               615                               620

Lys Arg Leu Ile Gly Glu Phe Asp Gln Gln Gln Ala Glu Ser Trp Ser
625                               630                               635                               640

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(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAATTAACCC TCATAAAGGG AAC

23

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAAAGTTTCA CCTTTTAGAA TCTAGAGCAA CTC

33

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAGGTGTCGA CGAGGAGCAG CGCTATGGGC TGTCGTGCGG AC

42

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTGTGGATCC TCATCACTAG GACCATGACT CTGCTTGCTG TTG

43

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 621 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ala	Ala	Leu	Lys	Glu	Asp	Arg	Ser	Tyr	Gly	Leu	Ser	Gly	Gly	Arg	1	5	10	15
Val	Ser	Asp	Gly	Ser	Lys	Val	Ser	Val	Phe	His	Val	Lys	Leu	Thr	Asp	20	25	30	
Ser	Ala	Ile	Arg	Ala	Phe	Glu	Ser	Tyr	Arg	Ala	Arg	Gln	Asp	Ser	Val	35	40	45	
Ser	Leu	Arg	Pro	Ser	Ile	Arg	Phe	Gln	Gly	Ser	Gln	Gly	His	Ile	Ser	50	55	60	
Ile	Pro	Gln	Pro	Asp	Cys	Pro	Ala	Glu	Ala	Arg	Thr	Phe	Ser	Phe	Tyr	65	70	75	80
Leu	Ser	Asn	Ile	Gly	Arg	Asp	Asn	Pro	Gln	Gly	Ser	Phe	Asp	Cys	Ile	85	90	95	
Gln	Gln	Tyr	Val	Ser	Ser	His	Gly	Glu	Val	His	Leu	Asp	Cys	Leu	Gly	100	105	110	
Ser	Ile	Gln	Asp	Lys	Ile	Thr	Val	Cys	Ala	Thr	Asp	Asp	Ser	Tyr	Gln	115	120	125	
Lys	Ala	Arg	Gln	Ser	Met	Ala	Gln	Ala	Glu	Glu	Glu	Ile	Arg	Ser	Arg	130	135	140	
Ser	Ala	Ile	Val	Ile	Lys	Ala	Gly	Gly	Arg	Tyr	Leu	Gly	Lys	Lys	Val	145	150	155	160
Gln	Phe	Arg	Lys	Pro	Ala	Pro	Gly	Ala	Thr	Asp	Ala	Val	Pro	Ser	Arg	165	170	175	
Lys	Arg	Ala	Thr	Pro	Ile	Asn	Leu	Ala	Ser	Ala	Ile	Arg	Lys	Ser	Gly	180	185	190	
Ala	Ser	Ala	Val	Ser	Gly	Gly	Ser	Gly	Val	Ser	Gln	Arg	Pro	Tyr	Arg	195	200	205	
Asp	Arg	Val	Ile	His	Leu	Leu	Ala	Leu	Arg	Pro	Tyr	Arg	Lys	Ala	Glu	210	215	220	
Leu	Leu	Leu	Arg	Leu	Gln	Lys	Asp	Gly	Leu	Thr	Gln	Ala	Asp	Lys	Asp	225	230	235	240
Ala	Leu	Asp	Gly	Ile	Leu	Gln	Gln	Val	Ala	Asn	Met	Ser	Ala	Lys	Asp	245	250	255	
Gly	Thr	Cys	Thr	Leu	Gln	Asp	Cys	Met	Tyr	Lys	Asp	Val	Gln	Lys	Asp				

260	265	270
Trp Pro Gly Tyr Ser Glu Gly Asp Gln Gln Leu Leu Lys Arg Val Leu		
275	280	285
Val Arg Lys Leu Cys Gln Pro Gln Ser Thr Gly Ser Leu Leu Gly Asp		
290	295	300
Pro Ala Ala Ser Ser Pro Pro Gly Glu Arg Gly Arg Ser Ala Ser Pro		
305	310	315
Pro Gln Lys Arg Leu Gln Pro Pro Leu Phe Ile Asp Pro Leu Ala Asn		
	325	330
Lys Lys Pro Arg Ile Ser His Phe Thr Gln Arg Ala Gln Pro Ala Val		
	340	345
Asn Gly Lys Leu Gly Val Pro Asn Gly Arg Glu Ala Leu Leu Pro Thr		
	355	360
Pro Gly Pro Pro Ala Ser Thr Asp Thr Leu Ser Ser Ser Thr His Leu		
	370	375
Pro Pro Arg Leu Glu Pro Pro Arg Ala His Asp Pro Leu Ala Asp Val		
385	390	395
Ser Asn Asp Leu Gly His Ser Gly Arg Asp Cys Glu His Gly Glu Ala		
	405	410
Ala Ala Pro Ala Pro Thr Val Arg Leu Gly Leu Pro Leu Leu Thr Asp		
	420	425
Cys Ala Gln Pro Ser Arg Pro His Gly Ser Pro Ser Arg Ser Lys Pro		
	435	440
Lys Lys Lys Ser Lys Lys His Lys Asp Lys Glu Arg Ala Ala Glu Asp		
450	455	460
Lys Pro Arg Ala Gln Leu Pro Asp Cys Ala Pro Ala Thr His Ala Thr		
465	470	475
Pro Gly Ala Pro Ala Asp Thr Pro Gly Leu Asn Gly Thr Cys Ser Val		
	485	490
Ser Ser Val Pro Thr Ser Thr Ser Glu Thr Pro Asp Tyr Leu Leu Lys		
	500	505
Tyr Ala Ala Ile Ser Ser Ser Glu Gln Arg Gln Ser Tyr Lys Asn Asp		
	515	520
Phe Asn Ala Glu Tyr Ser Glu Tyr Arg Asp Leu His Ala Arg Ile Glu		
530	535	540
Arg Ile Thr Arg Arg Phe Thr Gln Leu Asp Ala Gln Leu Arg Gln Leu		
545	550	555
Ser Gln Gly Ser Glu Glu Tyr Glu Thr Thr Arg Gly Gln Ile Leu Gln		
	565	570
Glu Tyr Arg Lys Ile Lys Lys Thr Asn Thr Asn Tyr Ser Gln Glu Lys		
	580	585
		590

His Arg Cys Glu Tyr Leu His Ser Lys Leu Ala His Ile Lys Arg Leu
 595 600 605
 Ile Ala Glu Tyr Asp Gln Arg Gln Leu Gln Ala Trp Pro
 610 615 620

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Trp Ile Arg Glu Tyr Pro Pro Ile Thr Ser Asp Gln Gln Arg Gln
 1 5 10 15
 Leu Tyr Lys Arg Asn Phe Asp Thr Gly Leu Gln Glu Tyr Lys Ser Leu
 20 25 30
 Gln Ser Glu Leu Asp Glu Ile Asn Lys Glu Leu Ser Arg Leu Asp Lys
 35 40 45
 Glu Leu Asp Asp Tyr Arg Glu Glu Ser Glu Glu Tyr Met Ala Ala Ala
 50 55 60
 Asp Glu Tyr Asn Arg Leu Lys Gln Val Lys Gly Ser Ala Asp Tyr Lys
 65 70 75 80
 Ser Lys Lys Asn His Cys Lys Gln Leu Lys Ser Lys Leu Ser His Ile
 85 90 95
 Lys Lys Met Val Gly Asp Tyr Asp Arg Gln Lys Thr
 100 105

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 297 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTCCACCGCT GCCTTCAACC TATCTGCCCA TCTCACATCC TCCTCAGATT GTAAATTCTA 60
 ACTCCAATC CCCTAGCACT CCAGAAGGCC GGGGGACTCA AGACCTACCT GTTGACAGTT 120

TTAGTCAAAA CGATAGTATC TATGAGGACC AGCAAGACAA ATATACCTCT AGGACTTCTC	180
TGGAAACCTT ACCCCCTGGT TCCGTTCTAC TAAAGTGTCC AAAGCCTATG GAAGAAAACC	240
ATTCAATGTC TCACAAAAAG TCCAAAAAGA AGTCTAAAAA ACATAAGGAA AAGGACC	297

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCAACCGAA GCACAAAAGT TATCAAACCC GGTGGACCAT ATGTAGGGAA AAGAGTGCAA	60
ATTCGGAAG CACCTCAAGC TGTTTCAGAT ACAGTTCCTG AGAGGAAAAG GTCAACCCCC	120
ATGAACCTG CAAATACAAT TCGAAAGACA CATAGCAGCA GCACCATCTC TCAGAGGCCA	180
TACAGGGACA GGGTGATTCA NTTACTGGCC CTGAAGGCCT ACAAGAAACC GGAGCTACTT	240
GCTAGACTCC AGAAAGATGG TGTCAATCAA AAAGACAAGA ACTCCCTGGG GAGGCAATTN	300
TTGCAACAGG TAGNCCAATC TGGATTTCTA AGGGACCTCT TCATATTACC TTAAAGG	358

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGCGNCGTNN TCGNCGGGCA CCCCAGGGAG TTTGAAGATG GCGGCGGGGG GGACAGGGGG	60
CCTNCGGGAG GAGCAGCGCT ATGGGCTGTC GTGCCGACG GCTGGGGCAG GACAACATCA	120
CCGTACTGCA TGTNAAAGCT TCACCGAGAC GGNCGATTCC GGGGCGGTTT GAGAACTTAC	180
CAGAGCCACA AGNNTTTNAA TTCCCTTTTC GGACCTTCAA TCCAGTTTCC AAGGACTCCA	240
CGGGCTTTGT NCAAAAATTT CCCAAAATG ATTCCCCTTC AATGGANAGT TCATAAATTT	300
TAAATTTTTA ATTTGTTCAA ATNTTGGGGN AAAGNCAAAC CTTCAAGGGC NAGTTTGGGA	360
CT	362

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AATTCGGCAC GAGCATGGTC CTAGAACTCT GCTTNGACCA GAAGATGTGA ATAAACTTAA 60
GCTTATTTAT TTAA AATTCC AAATGAGTNN NTCTAGNTTC TAAAAAGGTG AAAC TTTGGC 120
TGTGTAAAGT TTCAGTATTA GTAAACTTGA GTTACTTTNN CTTTTCATT TNACTTTGCT 180
TCCCTGCATT TCGAAGCTGC TCTTCTGGT CCTCCCCACC ACCCCACCCC CAAGACTTGT 240
GTTTGTTAAT AGAAATAATT TTTT TAGGTA TTGGGGATCC ATTGTCTATT ATTTCAAATC 300
AAGNTTTTTN TTTNTCCTCA AAAANCTTGT GGT TTTGTGA TTAGGAAATG GNTTTTTTAG 360
ATATTGGGGN TCCAGTGTCC NCACTTGAAA AGGTGGGNAG GGGTTTAAAA AANAGCANCA 420
GTAATNTGCA AGGTGNAATG NTTTTGGTNA ACGGANGCCA TTTTCCGACG TNCTTAA 477

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 178 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAACATTCTC CAGCTCTGGG ACCTCCANC TCAATTCCTT GGAATTNAT ACAAGATAAA 60
ATTACAGTGT GTGCACAAAC GACTCGTATC AAATGACACG AGAAANANTG ACCCAGGCAG 120
NGGAGGGAAT CCCGCAACCA ANGCAAAAA GTTATTCAAA CCCGGTGGGA CCATATNT 178

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GNCCTTTCTC CANTCTCAAA AGNGNTATCA CAATGTTTCAT GNAAGAAGTC TTACAAGAAT	60
ATCAGAAGAT AAAGCCAGTC TAGTCCCAAT TACCATGAAG NAAAAATACA GATGTGNAAT	120
ATCTTCATAA CAAGCTGGCT CACATCAAAA GGCTAATN	158

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATAAATAAGC TTAAGTTTAT TCACATCTTC TGGTCCAAGC AGAGTTCTAG GACCATGACT	60
CTGCTTGCTG TTGGTCAAAT TCACCTATTA GCCTTTTGAT GTGAGCCAGC TTGTTATGAA	120
GATATTCACA TCTGTATTTT TCTTCATGGT AATTGGGACT AGACTGCTTT ATCTTCTGAT	180
ATTCTTGTA GACTTCTTCA TGAACATTCT GATACTCTTT TGAGCCTGGA GAAAGGCGCT	240
TTCTTTGTGC ATCTAGTTTG ATAAATCTTC TAGCTACAGT CTCCATCCTG GCATGCAAAG	300
CTCTGTACTC ATCATACTCT GCATTGAAGT CATCCTTATA ATTCTGGCGT TGCTCATAGG	360
AGACGATAGC GATATATTTT ATCAAATAAT CTGGGAGTTC AATTGCTGAA GGGTCCATGG	420
AGGCAGTGCA ATCCTCTT	438

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCGNCCGCAG TGGANGGCTA GAGCGNAGCG CGCGGCGGCG GNCACCCCGG GGAGTTTAAG	60
ATGGCGGCNG GGGGGACAGG GGGCCTGCGG GAGGAGCAGC GCTATGGGCT GTCGTGCGGA	120
CGGCTGGGGC AGGACAACAT CACCGTACTG CATGTGAAGC TCACCGAGAC GGCGATCCGG	180

GCGCTCGAGA CTTACCAGAG CCACAAGAAT TTAATTCCTT TTCGACCTTC AATCCAGTTC	240
CAAGGACTCC ACGGGCTTGT CAAAATTCCC AAAAATGATC CCCTCAATGA AGTTCATAAC	300
TTTAACTTTT ATTTGTCAAA TGTGGGCAAA GACAACCCTC AGGGCAAGCT TTGACTGCAT	360
CCAGCAAACA TTCTCCAGCT CTGGAGCCTC CCAGCTCAAT TGCCTNGGGA TTTATACAAG	420
ATAAAATTAC AGTGTGTGCA ACAAACGACT CGTATCAGA	459

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TGGGATTCAA ATGACCATTT AGTGTGGTG GTACTCTGTT CGTCAGGTGA GATATTCGGG	60
CTTTTTTATT CATTAAAGGA TCAATAAACT CTGAATCCAA AAGCCGTTTC TGAGGAGAAG	120
ATACAGCATC TCTACTAGAA CATAACAGGAG ATTCTGAACG GCTGGTGCCT GTAGCATTCT	180
GAGACGGATT TAGTTTTCTA GAGAGCACTG ACTCCAATGA CCGTCTGTCT ATTTCACTGT	240
ATCCAGGCCA GTCTCTTTGA AGCTCTTTAA AAACATAATC CTTTAAGGGA TATGAGAGGT	300
CCTTAGAATT CAGATTGGCT AGCTGTTGCA GAATTGCTCC CAGGGAGTTC TTGTCTTTTT	360
GATTGACACC ATCTTTCTGG AGTCCTACAA GTAGCTCCGG GTTTCTTGTA GG	412

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAAATAAAG AACTTTGACA TTGAGACCAT GGAGGAGAAG GAGGAAGACC TTCAGAGAGA	60
AGAAACTGCC AAGCTGAGTA ATGCCAGTCC AAATCCCAAT GAAGGAGTTA AAGAAGGGTG	120
CACAGCCTCC ATGGAGCCTT CTTCAGCACT TGAACCTCCA GATTATTTGA TAAAATATAT	180
TGCTATTGTC TCTTATGAGC AACGCCAGAA TTACAAGGAT GACTTCAATG CTGAGTATGA	240

TGAATACAGA GCTTTGCATG CAAGGATGGA GACTGTAGCC AGGAGATTTA TTAAACTGGA	300
TGCACAAACGA AAACGCCTTT CTCCAGGTTC AAAAGAGTAC CAGAATGTTC ATGAAGAAGT	360
CTTACAGGAA TATCAGAAGA TCAAGCAGTC CAGTCCCAAT TACCATGAAG AAAAATACAG	420
ATGTGAATAT CTTCATAACA AGCTGGCTCA CATCAAAGAC TAATAGGTCG AATTGACCA	480
ACAGCAA	487

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 525 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCTTTGCATG CCAGGATGGA GACTGTAGCT AGAAGATTTA TCAAACTAGA TGCACAAAGA	60
AAGCGCCTTT CTCCAGGCTC AAAAGAGTAT CAGAATGTTC ATGAAGAAGT CTTACAAGAA	120
TATCAGAAGA TAAAGCAGTC TAGTCCCAAT TACCATGAAG AAAAATACAG ATGTGAATAT	180
CTTCATAACA AGCTGGCTCA CATCAAAGG CTAATAGGTG AATTGACCA ACAGCAAGCA	240
GAGTCATGGT CCTAGAACTC TGCTTGACC AGAAGATGTG AATAAACTTA AGCTTATTTA	300
TTTAAAATTC CAAATGAGTT GCTCTAGATT CTAAAAGGT GAACTTTGG CTGTTGAAAG	360
TTTCAGTATT AGTAAACTTN GAGTTACTTT TTCTTTTCCA TTTTACTTTG CTTCCCTGCA	420
TTTCGGAAGC TGCCTCTTTN CTGGGTCCTC NCCACTNGGG GCCAGCCCCC AAGNACTTGG	480
TGTTTTGGTT AATAGGNAAT AATTTTCTTT AAGGGAATTG GGGGA	525

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTAGTCAAAA TGGTAGCATC TTTGAGGACC AGCAAGAAAA ATATACCTCA AGGACTTGTC	60
TGGAACATT ACCCCCCAGC TCAGCTCTGC TAAAGTGTC AAAGCCCATG GAAGAAGAGC	120

ATCCAGTGTC TCACAAAAAG TCCAAAAAGA AGTCTAAAAA ACACAAGGAA AAGGACCAAA	180
TAAAGAAACT TGACATTGAG ACCATGGAGG AGAAGGAGGA AGACCTTCAG AGAGAAGAAA	240
CTGCCAAGCT GAGTAATGCC AGTCCAAATC CCAATGAAGG AGTTAAAGAA GGGTGCACAG	300
CCTCCATGGA GCCTTCTTCA GCACTTGAAC TCCCAGATTA TTTGATAAAA TATATTGCTA	360
TTGTCTCTTA TGAGCAACGC CAGAATTACA AGGATGACTT CAATGCTGAG TATGATGAAT	420
ACAGAGCTTT GCATGCAAGG ATGGAGACTG TAGCG	455

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 379 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TCACCTTACTG GCCCTGAAGG CTACAAGAAA CCGGAGCTAC TTGCTAGACT CCAGAAAGAT	60
GGTGTCATC AAAAAGACAA GAACTCCCTG GGAGCAATTC TGCAACAGGT AGCCAATCTG	120
AATTCTAAGG ACCTCTCATA TACCTTAAAG GATTATGTTT TTAAAGAGCT TCAAAGAGAC	180
TGGCCTGGNT ACAGTGAAAT AGACAGACGG TCATTGGAGT CAGTGCTCTC TAGAAACTA	240
AATCCGTCTC AGAATGCTAC AGGCACCAGC CTNTCAGAAT CTCCTGTATG TTCTAGTAGA	300
GATGCTGTAT CTTCTCCTCA GGAAACGGCT TTTGGGTTTC AGAGTTTATT TGATCCCTTT	360
AATGGANTTA AAAAAGGCT	379

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 519 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

NTCACTTACT GGCCCTGAAG CTANCAAGAA ACCGGAGCTA CTTGCTAGAC TCCAGAAAGA	60
TGGTGTCAT CAAAAGACA AGAACTCCCT GGGAGCAATT CTGCAACAGG TAGCCAATCT	120
GAATTCTAAG GACCTCTCAT ATACCTTAAA GGATTATGTT TTTAAAGAGC TTCAAAGAGA	180

CTGGCCTGGG ATACAGTGAA ATAGACAGAC GGTCAATTGGA GTCAGTGCTC TCTAGAAAAC	240
TAAATCCGTC TCAGAATGCT ACAGGCACCA GCGTTTCAGA ATCTCCTGTA TGTTCCTAGTA	300
GGAGATGCTG TATCTTCTCC TCAGGAAACG GCTTTTGGGT TCAGGAGTTT ATTTGATCCN	360
TTTAATGGAT TAAAAAAGGC CCCGATTATT CTTACCTGG ACGGAACAGA GTTACCNCCC	420
AACATTAATG GGTCCNTTTG GATTCCCACC AGTGGAAAAT TGGGTGGCGG GCTTNCCCAT	480
TGCCCCTGNG GGTGGTGGCN TTCCCCACCC TTNCACCGG	519

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTCCACCGCT GCCTTCAACC TATCTGCCCA TCTCACATCC TCCTCAGATT GTAAATTCTA	60
ACTCCAATC CCCTAGCACT CCAGAAGGCC GGGGGACTCA AGACCTACCT GTTGACAGTT	120
TTAGTCAAAA CGATAGTATC TATGAGGACC AGCAAGACAA ATATACCTCT AGGACTTCTC	180
TGGAAACCTT ACCCCCTGGT TCCGTTCTAC TAAAGTGTC AAAGCCTATG GAAGAAAACC	240
ATTCAATGTC TCACAAAAG TCCAAAAGA AGTCTAAAAA ACATAAGGAA AAGGACC	297

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGCAACCGAA GCACAAAAGT TATCAAACCC GGTGGACCAT ATGTAGGGAA AAGAGTGCAA	60
ATTCGGAAAG CACCTCAAGC TGTTCAGAT ACAGTTCCTG AGAGGAAAAG GTCAACCCCC	120
ATGAACCTG CAAATACAAT TCGAAAGACA CATAGCAGCA GCACCATCTC TCAGAGGCCA	180
TACAGGGACA GGGTGATTCA NTTACTGGCC CTGAAGGCCT ACAAGAAACC GGAGCTACTT	240
GCTAGACTCC AGAAAGATGG TGTCATCAA AAAGACAAGA ACTCCCTGGG GAGGCAATTN	300

TTGCAACAGG TAGNCCAATC TGGATTTCTA AGGGACCTCT TCATATTACC TTAAAGG 358

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 285 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTTTGTGAGA CATTGAATGG TTTTCTTCCA TAGGCTTTGG AACTTTTAGT AGAACGGAAC 60
CAGGGGGTAA GGTTTCCAGA GAAGTCCTAG AGGTATATTT GTCTTGCTGG TCCTCATAGA 120
TACTATCGTT TTGACTAAAA CTNTCAACAG GTAGGTCTTG AGTCCCCCGG CCTTCTGGAG 180
TGCTAGGGGA GTTGGAGTTA GAATTTACAA TCTGAGGAGG ATGTGAGATG GGCAGATAGG 240
TTGAAGGCAG CGGTGGAGGG GTGGGGATGG CAGCAGCCCA GGGGG 285

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 431 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TTTATTCCAA ACAGCATCAT CTACAACTCA TAATCGCAGG CTCCTCCAGT TCATTTAACA 60
CAGAAAGCAG GCTTTTTTCT CTTTCCCAT TTAAACAAAT GTAAATACC TTCATTGGGA 120
TTTGGACTGG CATTACTCAG CTTGGCAGTT TCTTCTCTCT GAAGGTCTTC CTCCTTCTCC 180
TCCATGGTCT CAATGTCAAG TTTCTTTATT TGGTCCTTTT CTTGTGTTT TTTAGACTTC 240
TTTTTGGACT TTTTGTGAGA CACTGGATGC TCTTCTTCCA TGGGCTTTGG AACTTTTAGC 300
AGAGTGAGCT GGGGGGTAAAT GTTTCAGAC AAGTCCTTGA GGTATATTTT TCTTGCTGGT 360
CCTCAAAGAT GCTACCATTT TGAATAAAC TGCAACAGG CAGGTCTTGA GTCCAGGCC 420
TTCTGGAGTG C 431

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 196 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CACCGAGACG GCGATCCGGG CGCTCGAGAC TTACCAGAGC CACAAGAATT TAATTCCTTT 60
TCGACCTTCA ATCCAGTTCC AAGGACTCCA CGGGCTTGTC AAAATTCCCA AAAATGATCC 120
CCTCAATGAA GTTCATAACT TTAACCTTTA TTTGTCAAAT GTGGGCAAAG ACAACCCTCA 180
GGGGAGCTTG GGCTGC 196

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 197 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ACCATCTCTC AGAGGCCATA CAGGGACAGG GTGATTCAC TACTGGCCCT GAAGGCNTAC 60
AAGAAACCGG AGCTACTTGC TAGACTCCAG AAAGATGGTG TCAATCAAAA AGACAAGAAC 120
TCCCTGGGAG CAATTCTGCA ACAGGTAGCC AATCTGAATN CTAAGGACCT CNTCATATAC 180
CTTAAAGGAT TATGTTT 197

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GCGCCCGGCA GTGGAGGCTA GAGCCGCAGC GCGCGGCGGG CGGACACCGC CGGGGAGGTT 60
TAAGAGTGGC GGCTGGGGGG GACAGGGGGG CCTGCAGGGA GGAGCAGCGC TATGGGCTGT 120
CGTGCGGACG GCGTGGGGCA GGACAACATC ACCGTACTGC ATGTGAAGCT CACCGAGACG 180

GCGATCCGGG CGCTCGAGAC TTACCAGAGC CACAAGAATT TAATTCCTTT TCGACCTTCA 240
ATCCAGTTCC AAGGACTCCA CGGGGTGAGT ACTCTTATTG ATTTAACAAA CAAATCTAAT 300
GTTCTTGCAC GCTATTCAAC TTTTAAATC CGTTTTTCACT TGACCCTT 348

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGGAATTTTAA ATAAATAAGC TTAAGTTTAT TCACATCTNC TGGTCCAAGC AGAGTTCTAG 60
GACCATGACT CTGCTTGCTG TTGGTCAAAT TCACCTATTA GCCTTTNGAT GTGAGCCAGC 120
TTGTTATGAA GATATTCACA TCTGTATTTT NCTTCATGGT AATTGGGACT AGACTGCTTT 180
ATCT 184

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TCCTAGAACT CTGCTTGGAC CAGAAGATGT GAATAAACTT AAGCTTATTT ATTTAAAATC 60
ACAAATGAGT TGCTCTAGAT TCTAAAAGGG TGAAACTTTG ACTGTTGAAA GTTTAAGTAT 120
TAGTAAACTT GAGTTACTTT TTCTTTCAAA TTTCACTCCG CTTCCCTGCA TTTCGAAGCT 180
GCTCTTTCTG GTCCTACCCA CCACCCACC AACAAGACTT GTGTTTGTTA ATAGAAATAA 240
TTTATCAAGG TATTGGGGAT CCATTGTCTA TATTTAAAC 280

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

AAC TAGCAGT CCCTTTGGGC CAATTGATGT AATTATTTTC AGTGTAATC CNAAAGGTTG	60
CCTGTTTTAN GNTAGGAGAT GATAGTAAAA ATACCTAATG CTCTGTTTTT ATACCTCATA	120
CTAGGTAGCC AATCTGAATT CTAAGGACCT CTCATATACC TTAAAGGATT ATGTTTNTAA	180
AGAGCTTCAA AGAGACTGGC CTGGATACAG TGAAATAGAC AGACGGTCAT TGGAGTCATG	240
TGCTCTCTAG GTGAA	255

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3974 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGTACCTAAG TGAGTAGGGC GTCCGATCGA CGGACGCCTT TTTTGAAT TCGTAATCAT	60
GGTCATAGCT GTTTCCTGTG TGAAATTGTT ATCCGCTCAC AATTCCACAC AACATACGAG	120
CCGGAAGCAT AAAGTGTAAG GCCTGGGGTG CCTAATGAGT GAGCTAACTC ACATTAATTG	180
CGTTGCGCTC ACTGCCCCGCT TTCCAGTCGG GAAACCTGTC GTGCCAGCTG CATTAATGAA	240
TCGGCCAACG CGCGGGGAGA GCGGGTTTGC GTATTGGGCG CTCTTCGCT TCCTCGCTCA	300
CTGACTCGCT GCGCTCGGTC GTTCGGCTGC GCGGAGCGGT ATCAGCTCAC TCAAAGGCGG	360
TAATACGGTT ATCCACAGAA TCAGGGGATA ACGCAGGAAA GAACATGTGA GCAAAAGGCC	420
AGCAAAAGGC CAGGAACCGT AAAAAGGCCG CGTTGCTGGC GTTTTCCAT AGGCTCCGCC	480
CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG GTGGCGAAAC CCGACAGGAC	540
TATAAAGATA CCAGGCGTTT CCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTCCGACCC	600
TGCCGCTTAC CGGATACCTG TCCGCCTTTC TCCCTTCGGG AAGCGTGGCG CTTTCTCATA	660
GCTCACGCTG TAGGTATCTC AGTTCGGTGT AGGTCGTTCT CTCCAAGCTG GGCTGTGTGC	720
ACGAACCCCC CGTTCAGCCC GACCGCTGCG CCTTATCCGG TAACTATCGT CTTGAGTCCA	780
ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC TGATAACAGG ATTAGCAGAG	840
CGAGGTATGT AGGCGGTGCT ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA	900

GAAGAACAGT	ATTTGGTATC	TGCGCTCTGC	TGAAGCCAGT	TACCTTCGGA	AAAAGAGTTG	960
GTAGCTCTTG	ATCCGGCAAA	CAAACCACCG	CTGGTAGCGG	TGGTTTTTTT	GTTTGCAAGC	1020
AGCAGATTAC	GCGCAGAAAA	AAAGGATCTC	AAGAAGATCC	TTTGATCTTT	TCTACGGGGT	1080
CTGACGCTCA	GTGGAACGAA	AACTCACGTT	AAGGGATTTT	GGTCATGAGA	TTATCGTCGA	1140
CAATTCGCGC	GCGAAGGCGA	AGCGGCATGC	ATTTACGTTG	ACACCATCGA	ATGGTGCAAA	1200
ACCTTTCGCG	GTATGGCATG	ATAGCGCCCG	GAAGAGAGTC	AATTCAGGGT	GGTGAATGTG	1260
AAACCAGTAA	CGTTATACGA	TGTCGCAGAG	TATGCCGGTG	TCTCTTATCA	GACCGTTTCC	1320
CGCGTGGTGA	ACCAGGCCAG	CCACGTTTCT	GCGAAAACGC	GGGAAAAAGT	GGAAGCGGCG	1380
ATGGCGGAGC	TGAATTACAT	TCCCAACCGC	GTGGCACAAC	AACTGGCGGG	CAAACAGTCG	1440
TTGCTGATTG	GCGTTGCCAC	CTCCAGTCTG	GCCCTGCACG	CGCCGTCGCA	AATTGTCGCG	1500
GCGATTAAAT	CTCGCGCCGA	TCAACTGGGT	GCCAGCGTGG	TGGTGTGCGAT	GGTAGAACGA	1560
AGCGGCGTCG	AAGCCTGTAA	AGCGGCGGTG	CACAATCTTC	TCGCGCAACG	CGTCAGTGGG	1620
CTGATCATTG	ACTATCCGCT	GGATGACCAG	GATGCCATTG	CTGTGGAAGC	TGCCTGCACT	1680
AATGTTCCGG	CGTTATTTCT	TGATGTCTCT	GACCAGACAC	CCATCAACAG	TATTATTTTC	1740
TCCCATGAAG	ACGGTACGCG	ACTGGGCGTG	GAGCATCTGG	TCGCATTGGG	TCACCAGCAA	1800
ATCGCGCTGT	TAGCGGGCCC	ATTAAGTTCT	GTCTCGGCGC	GTCTGCGTCT	GGCTGGCTGG	1860
CATAAATATC	TCACTCGCAA	TCAAATTCAG	CCGATAGCGG	AACGGGAAGG	CGACTGGAGT	1920
GCCATGTCCG	GTTTTCAACA	AACCATGCAA	ATGCTGAATG	AGGGCATCGT	TCCCACTGCG	1980
ATGCTGGTTG	CCAACGATCA	GATGGCGCTG	GGCGCAATGC	GCGCCATTAC	CGAGTCCGGG	2040
CTGCGCGTTG	GTGCGGATAT	CTCGGTAGTG	GGATACGACG	ATACCGAAGA	CAGCTCATGT	2100
TATATCCCGC	CGTTAACCAC	CATCAAACAG	GATTTTCGCC	TGCTGGGGCA	AACCAGCGTG	2160
GACCGCTTGC	TGCAACTCTC	TCAGGGCCAG	GCGGTGAAGG	GCAATCAGCT	GTTGCCCGTC	2220
TCACTGGTGA	AAAGAAAAAC	CACCCTGGCG	CCCAATACGC	AAACCGCCTC	TCCCCGCGCG	2280
TTGGCCGATT	CATTAATGCA	GCTGGCACGA	CAGGTTTCCC	GACTGGAAAG	CGGGCAGTGA	2340
GCGCAACGCA	ATTAATGTAA	GTTAGCGCGA	ATTGTGCGAC	AAAGCGGCCA	TCGTGCCTCC	2400
CCACTCCTGC	AGTTCGGGGG	CATGGATGCG	CGGATAGCCG	CTGCTGGTTT	CCTGGATGCC	2460
GACGGATTTG	CACTGCCGGT	AGAAC'TCCGC	GAGGTCGTCC	AGCCTCAGGC	AGCAGCTGAA	2520
CCAAC'TCGCG	AGGGGATCGA	GCCCGGGGTG	GGCGAAGAAC	TCCAGCATGA	GATCCCCGCG	2580
CTGGAGGATC	ATCCAGCCGG	CGTCCCGGAA	AACGATTCCG	AAGCCCAACC	TTTCATAGAA	2640
GGCGGCGGTG	GAATCGAAAT	CTCGTGATGG	CAGGTTGGGC	GTCGCTTGGT	CGGTCATTTC	2700
GAACCCAGAG	GTCCCGCTCA	GAAGAACTCG	TCAAGAAGGC	GATAGAAGGC	GATGCGCTGC	2760

GAATCGGGAG CGGCGATACC GTAAAGCACG AGGAAGCGGT CAGCCCATTG GCCGCCAAGC	2820
TCTTCAGCAA TATCACGGGT AGCCAACGCT ATGTCCTGAT AGCGGTCCGC CACACCCAGC	2880
CGGCCACAGT CGATGAATCC AGAAAAGCGG CCATTTTCCA CCATGATATT CGGCAAGCAG	2940
GCATCGCCAT GGGTCACGAC GAGATCCTCG CCGTCGGGCA TGCGCGCCTT GAGCCTGGCG	3000
AACAGTTCCG CTGGCGCGAG CCCCTGATGC TCTTCGTCCA GATCATCCTG ATCGACAAGA	3060
CCGGCTTCCA TCCGAGTACG TGCTCGCTCG ATGCGATGTT TCGCTTGGTG GTCGAATGGG	3120
CAGGTAGCCG GATCAAGCGT ATGCAGCCGC CGCATTGCAT CAGCCATGAT GGATACTTTC	3180
TCGGCAGGAG CAAGGTGAGA TGACAGGAGA TCCTGCCCCG GCACTTCGCC CAATAGCAGC	3240
CAGTCCCTTC CCGCTTCAGT GACAACGTCG AGCACAGCTG CGCAAGGAAC GCCCGTCGTG	3300
GCCAGCCACG ATAGCCGCGC TGCTCGTCC TGCAATTGAT TCAGGGCACC GGACAGGTCG	3360
GTCTTGACAA AAAGAACCGG GCGCCCCTGC GCTGACAGCC GGAACACGGC GGCATCAGAG	3420
CAGCCGATTG TCTGTTGTGC CCAGTCATAG CCGAATAGCC TCTCCACCCA AGCGGCCGGA	3480
GAACCTGCGT GCAATCCATC TTGTTCAATC ATGCGAAACG ATCCTCATCC TGTCTCTTGA	3540
TCAGATCTTG ATCCCCTGCG CCATCAGATC CTTGGCGGCA AGAAAGCCAT CCAGTTTACT	3600
TTGCAGGGCT TCCCAACCTT ACCAGAGGGC GCCCCAGCTG GCAATTCCGG TTCGCTTGCT	3660
GTCCATAAAA CCGCCCAGTC TAGCTATCGC CATGTAAGCC CACTGCAAGC TACCTGCTTT	3720
CTCTTTGCGC TTGCGTTTTT CTTGTCCAG ATAGCCCAGT AGCTGACATT CATCCGGGGT	3780
CAGCACCGTT TCTGCGGACT GGCTTTCTAC GTGTTCCGCT TCCTTTAGCA GCCCTTGCGC	3840
CCTGAGTGCT TGCGGCAGCG TGAAGCTTAA AAAACTGCAA AAAATAGTTT GACTTGTGAG	3900
CGGATAACAA TTAAGATGTA CCCAATTGTG AGCGGATAAC AATTTACAC ATTAAGAGG	3960
AGAAATTACA TATG	3974

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

AAGCTTAAAA AACTGCAAAA AATAGTTTGA CTTGTGAGCG GATAACAATT AAGATGTACC	60
CAATTGTGAG CGGATAACAA TTTACACAT TAAAGAGGAG AAATTACATA TG	112